James Y Dai

List of Publications by Year in descending order

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Version: 2024-02-01

		687363	377865
41	1,269	13	34
papers	citations	h-index	g-index

43	43	43	3443
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
2	Two-stage testing procedures with independent filtering for genome-wide gene-environment interaction. Biometrika, 2012, 99, 929-944.	2.4	148
3	FCGR2C polymorphisms associate with HIV-1 vaccine protection in RV144 trial. Journal of Clinical Investigation, 2014, 124, 3879-3890.	8.2	99
4	Simultaneously Testing for Marginal Genetic Association and Gene-Environment Interaction. American Journal of Epidemiology, 2012, 176, 164-173.	3.4	67
5	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
6	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780.	1.9	35
7	A Multiple-Testing Procedure for High-Dimensional Mediation Hypotheses. Journal of the American Statistical Association, 2022, 117, 198-213.	3.1	30
8	Esophageal Adenocarcinoma and Its Rare Association with Barrettâ€™s Esophagus in Henan, China. PLoS ONE, 2014, 9, e110348.	2.5	25
9	A Newly Identified Susceptibility Locus nearFOXP1Modifies the Association of Gastroesophageal Reflux with Barrett's Esophagus. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1739-1747.	2.5	24
10	Estimating the Efficacy of Preexposure Prophylaxis for HIV Prevention Among Participants With a Threshold Level of Drug Concentration. American Journal of Epidemiology, 2013, 177, 256-263.	3.4	21
11	Semiparametric Estimation Exploiting Covariate Independence in Twoâ€Phase Randomized Trials. Biometrics, 2009, 65, 178-187.	1.4	19
12	Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. Human Genomics, 2015, 9, 22.	2.9	19
13	Diagnostics for Pleiotropy in Mendelian Randomization Studies: Global and Individual Tests for Direct Effects. American Journal of Epidemiology, 2018, 187, 2672-2680.	3.4	18
14	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. British Journal of Cancer, 2018, 118, 1639-1647.	6.4	16
15	DNA methylation and cis-regulation of gene expression by prostate cancer risk SNPs. PLoS Genetics, 2020, 16, e1008667.	3.5	15
16	Case-only method for cause-specific hazards models with application to assessing differential vaccine efficacy by viral and host genetics. Biostatistics, 2014, 15, 196-203.	1.5	13
17	Association between post-treatment circulating biomarkers of inflammation and survival among stage IIâ€“III colorectal cancer patients. British Journal of Cancer, 2021, 125, 806-815.	6.4	12
18	SHARE: an adaptive algorithm to select the most informative set of SNPs for candidate genetic association. Biostatistics, 2009, 10, 680-693.	1.5	11

#	Article	IF	Citations
19	Germline variation in the insulin-like growth factor pathway and risk of Barrettâ€™s esophagus and esophageal adenocarcinoma. Carcinogenesis, 2021, 42, 369-377.	2.8	11
20	Robust Estimation for Secondary Trait Association in Case-Control Genetic Studies. American Journal of Epidemiology, 2014, 179, 1264-1272.	3.4	10
21	Mendelian Randomization Studies for a Continuous Exposure Under Case-Control Sampling. American Journal of Epidemiology, 2015, 181, 440-449.	3.4	9
22	Case-only Approach to Identifying Markers Predicting Treatment Effects on the Relative Risk Scale. Biometrics, 2018, 74, 753-763.	1.4	9
23	Pharmacokinetics and Pharmacodynamics of Tenofovir Reduced-Glycerin 1% Gel in the Rectal and Vaginal Compartments in Women: A Cross-Compartmental Study With Directly Observed Dosing. Journal of Acquired Immune Deficiency Syndromes (1999), 2018, 78, 175-182.	2.1	9
24	A unified procedure for meta-analytic evaluation of surrogate end points in randomized clinical trials. Biostatistics, 2012, 13, 609-624.	1.5	7
25	Testing concordance of instrumental variable effects in generalized linear models with application to Mendelian randomization. Statistics in Medicine, 2014, 33, 3986-4007.	1.6	7
26	Constrained Score Statistics Identify Genetic Variants Interacting with Multiple Risk Factors in Barrettâ€™s Esophagus. American Journal of Human Genetics, 2016, 99, 352-365.	6.2	7
27	Quantification of multiple tumor clones using gene array and sequencing data. Annals of Applied Statistics, 2017, 11, 967-991.	1.1	7
28	EMeth: An EM algorithm for cell type decomposition based on DNA methylation data. Scientific Reports, 2021, 11, 5717.	3.3	7
29	Whole-genome sequencing of esophageal adenocarcinoma in Chinese patients reveals distinct mutational signatures and genomic alterations. Communications Biology, 2018, 1, 174.	4.4	6
30	Genetically Predicted Circulating C-Reactive Protein Concentration and Colorectal Cancer Survival: A Mendelian Randomization Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1349-1358.	2.5	6
31	Identifying Disease-Associated Copy Number Variations by a Doubly Penalized Regression Model. Biometrics, 2018, 74, 1341-1350.	1.4	5
32	Case-Only Trees and Random Forests for Exploring Genotype-Specific Treatment Effects in Randomized Clinical Trials with Dichotomous End Points. Journal of the Royal Statistical Society Series C: Applied Statistics, 2019, 68, 1371-1391.	1.0	5
33	Interactive decision support for esophageal adenocarcinoma screening and surveillance. BMC Gastroenterology, 2019, 19, 109.	2.0	4
34	TwoPhaseInd: an R package for estimating geneâ€“treatment interactions and discovering predictive markers in randomized clinical trials. Bioinformatics, 2016, 32, 3348-3350.	4.1	3
35	Editorial: Mendelian Randomization Analysis Identifies Body Mass Index and Fasting Insulin as Potential Causal Risk Factors for Pancreatic Cancer Risk. Journal of the National Cancer Institute, 2017, 109, .	6.3	3
36	Best linear inverse probability weighted estimation for twoâ€phase designs and missing covariate regression. Statistics in Medicine, 2019, 38, 2783-2796.	1.6	3

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37	Group association test using a hidden Markov model. Biostatistics, 2016, 17, 221-234.	1.5	2
38	Genetic variants associated with circulating Câ€reactive protein levels and colorectal cancer survival: Sexâ€specific and lifestyle factors specific associations. International Journal of Cancer, 2022, 150, 1447-1454.	5.1	2
39	Case-only Methods Identified Genetic Loci Predicting a Subgroup of Men with Reduced Risk of High-grade Prostate Cancer by Finasteride. Cancer Prevention Research, 2019, 12, 113-120.	1.5	1
40	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	1
41	A risk variant for Barrettâ€™s esophagus and esophageal adenocarcinoma at chr8p23.1 affects enhancer activity and implicates multiple gene targets. Human Molecular Genetics, 2022, 31, 3975-3986.	2.9	1